

Length of GAP-2/7.10.93 komplett: 330 bp; Listed from: 2 to: 330;
Translated from: 11 to: 151 (Entire region);
Genetic Code used: Universal; Don. 7. Okt 1993 15:25 Uhr

Primer

Eco RI → |
Xba I | → from here cDNA

Frame 2 (N)
CEAT TCT AGA Q R I M D Y IY E T S S Q C S K
CAG CGG ATC ATG CAT TACITAT GAG ACC AGC AGC CAG TGC TCC AAG
10 19 28 37 46 55

P G I V F I T K R G H S V C T N P S D K
CCC GCA ATT GTC TTC ATC ACC AAA AGG GGC CAT TCC GTC TGT ACC AAC CCC ACT GAC AAG
64 73 82 91 100 109

(E) | → 3'-untranslated
W V Q D Y I K D H K E N STOP region
TGG GTC CAG GAC TAT ATC AAG GAC ATG AAG GAG AAC TGA GTG ACC CAG AAG GGG TGG CGA
124 133 142 151 160 169

AGG CAC AGC TCA GAG ACA TAA AGA GAA GAT GCC AAG GCC CCC TCC TCC ACC CAC CCC TAA
184 193 202 211 220 229

polyadenylation signal

CTC TCA GCC CCA GTC ACC CTC TTG GAG CTT CCC TCC TTT GAA TTA AAG ACC ACT CAT GCT
244 253 262 271 280 289

→ poly(A) tail or primer UNIP-2

Eco RI
Xba I
Sac I
CTT CAA AAA AAA AAA AAA AAT GAG CTC TAG AAT TC
304 313 322

Amino acid modifications in the peptide sequence
are given in parentheses.

Figure 1

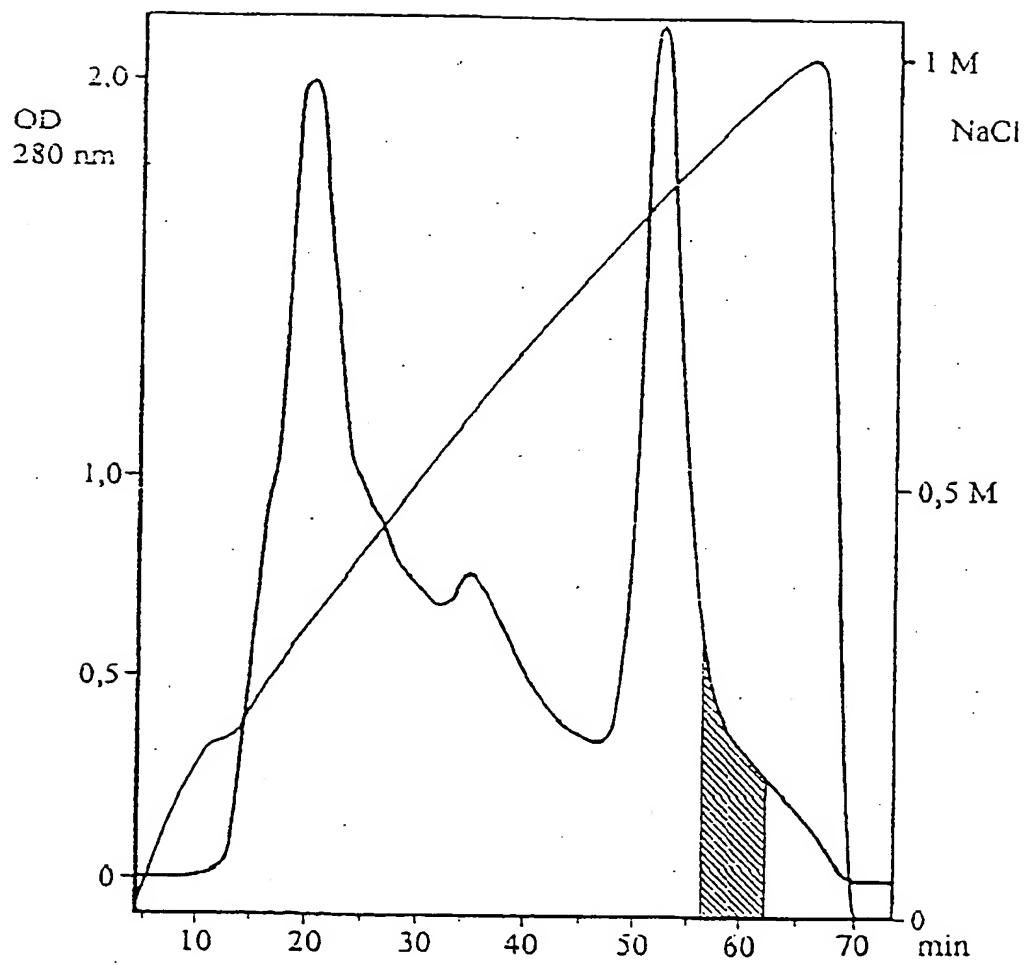


Figure 2

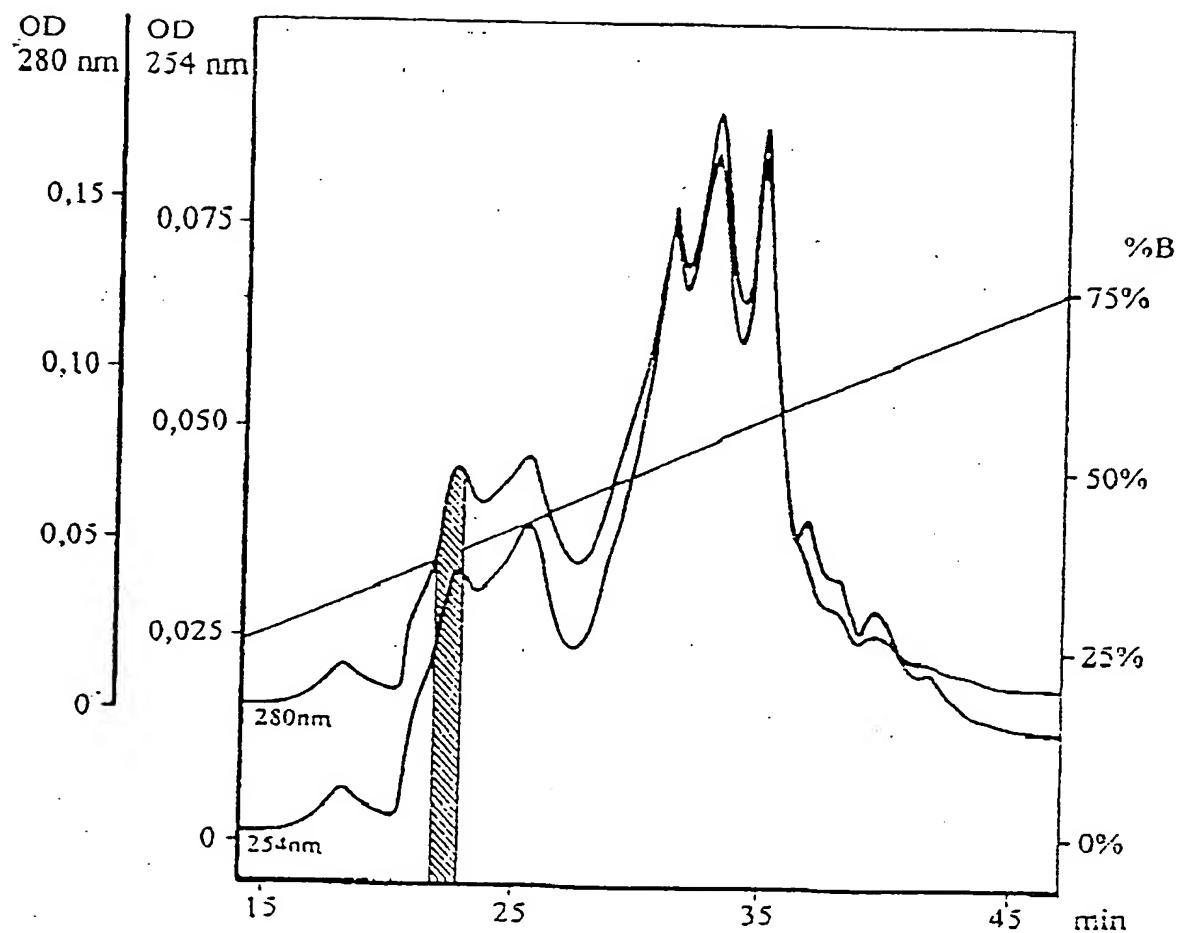


Figure 3a

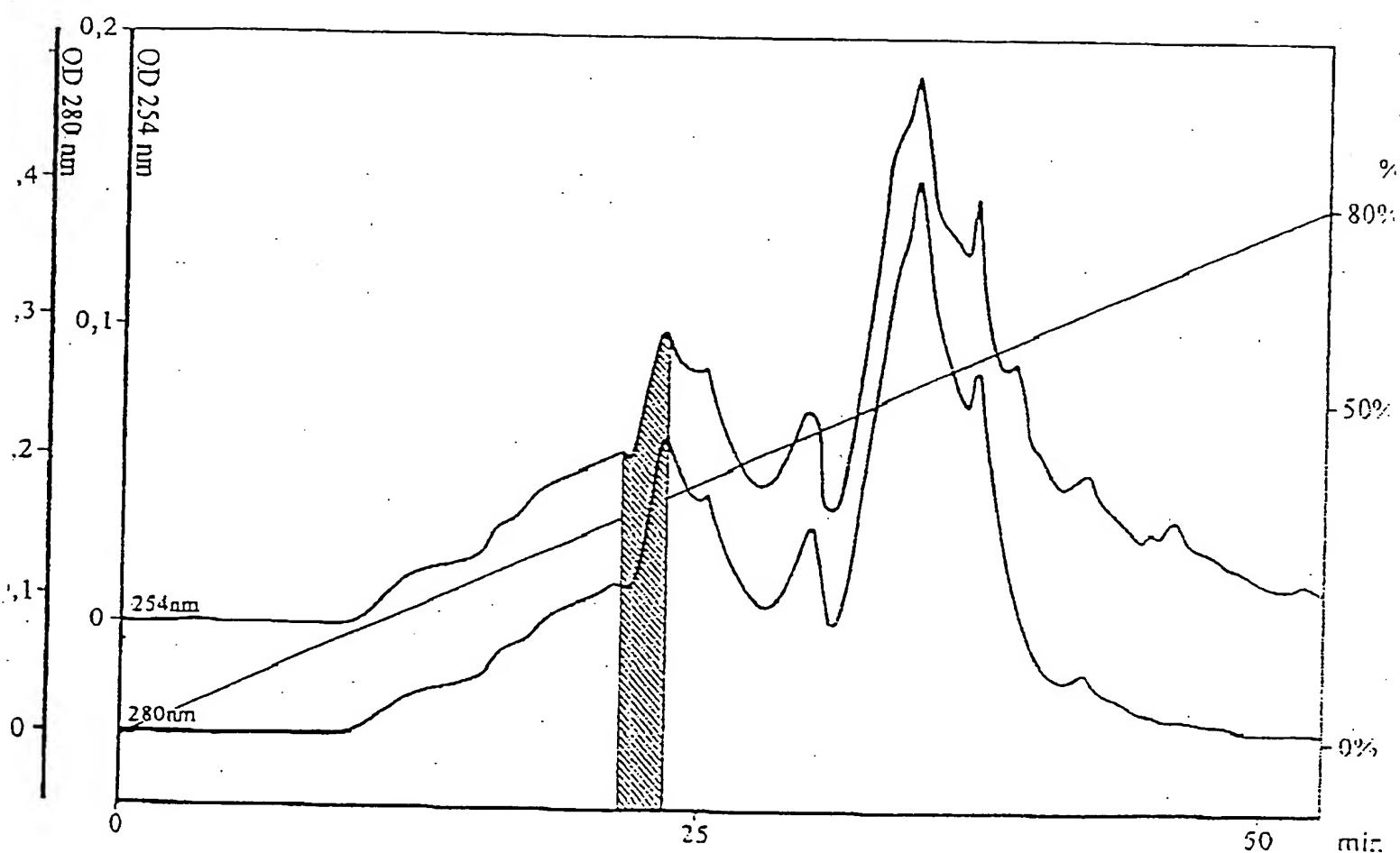


Figure 3b

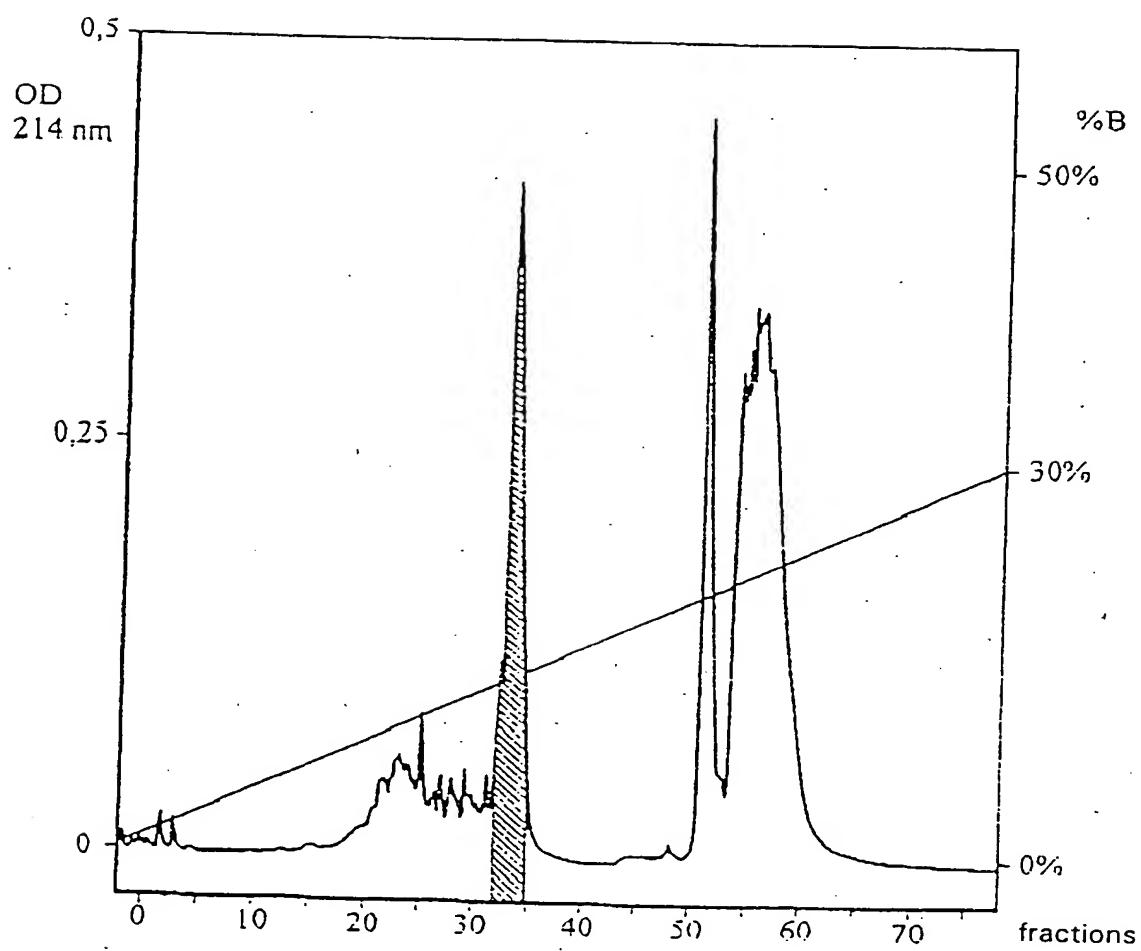


Figure 4